

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/687,879A
Source: IFWO
Date Processed by STIC: 12-29-04

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 12/29/2004

PATENT APPLICATION: US/10/687,879A

TIME: 15:28:25

Input Set : A:\2004-12-07 2428-0125P.ST25.txt

Output Set: N:\CRF4\12292004\J687879A.raw

```

3 <110> APPLICANT: LAMBERT, Bart
4     JANSENS, Stefan
5     van AUDENHOVE, Katrien
6     PEFEROEN, Marnix
8 <120> TITLE OF INVENTION: New Bacillus Thuringiensis Strains and Their Insecticidal
9     Proteins
11 <130> FILE REFERENCE: 2428-0125P
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/687,879A
14 <141> CURRENT FILING DATE: 2003-10-20
16 <150> PRIOR APPLICATION NUMBER: US 09/220,806
17 <151> PRIOR FILING DATE: 1998-12-28
19 <150> PRIOR APPLICATION NUMBER: US 08/379,656
20 <151> PRIOR FILING DATE: 1995-03-23
22 <160> NUMBER OF SEQ ID NOS: 5
24 <170> SOFTWARE: PatentIn version 3.2
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 19
28 <212> TYPE: DNA
29 <213> ORGANISM: Bacillus thuringiensis
32 <220> FEATURE:
33 <221> NAME/KEY: misc_feature
34 <222> LOCATION: (1)..(19)
35 <223> OTHER INFORMATION: This probe is a part of the coding DNA strand of the cryIG
gene,
36     described by Smulevitch et al. (1991). This probe is used to
37     isolate the bTS02618A gene from its containing strain.
39 <400> SEQUENCE: 1
40 ttctgtacta ttgattgta
43 <210> SEQ ID NO: 2
44 <211> LENGTH: 1561
45 <212> TYPE: DNA
46 <213> ORGANISM: Bacillus thuringiensis
49 <220> FEATURE:
50 <221> NAME/KEY: misc_feature
51 <222> LOCATION: (1)..(1561)
52 <223> OTHER INFORMATION: Contains the translation initiation codon of the bTS02618A
gene.
54 <220> FEATURE:
55 <221> NAME/KEY: misc_feature
56 <222> LOCATION: (708)..(708)
57 <223> OTHER INFORMATION: n = a, c, g, t, any, unknown, or other.
59 <400> SEQUENCE: 2
60 aaaaagaaat aggaataaat actatccatt ttttcaagaa atattttttt attagaaagg      60
62 aatctttctt acacgggaaa atcctaagat tgagagtaaa gatatatata tataaatata      120

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64 ataaagagtt tgtcaggatt ttgaaagat atgatatgaa catgcactag atttatagta 180

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66 taggaggaaa aagtatgaat cgaaataatc aaaaatgaata tgaaattatt gatgcccccc 240
68 attgtgggtg tccatcagat gacgatgtga ggtatccttt ggcaagtgc ccaaatgcag 300
70 cgttacaaaa tatgaactat aaagattact tacaaatgac agatgaggac tacactgatt 360
72 cttatataaa tcctagttaa tctattagtgt gtagagatgc agttcagact gcgcttactg 420
74 ttgttggggag aatactcggg gcttttaggtg ttccgttttc tggacaaata gtgagttttt 480
76 atcaattcct tttaaataca ctgtggccag ttaatgatac agctatatgg gaagctttca 540
78 tgcgacaggt ggaggaactt gtcaatcaac aaataacaga atttgcaaga aatcaggcac 600
80 ttgcaagatt gcaaggatta ggagactctt ttaatgtata tcaacgttcc cttcaaaatt 660
W--> 82 ggttggctga tcgaaatgat acacgaaatt taagtgttgt tcgtgctnaa tttatagctt 720
84 tagaccttga ttttggttaat gctattccat tgtttgcagt aaatggacag caggttccat 780
86 tactgtcagt atatgcacaa gctgtgaatt tacatttgtt attattaaaa gatgcatctc 840
88 tttttggaga aggatgggga ttcacacagg gggaaatttc cacatattat gaccgtcaat 900
90 tggaaactaac cgctaagtac actaattact gtgaaacttg gtataataca ggtttagatc 960
92 gtttaagagg aacaaatact gaaagttggt taagatatca tcaattccgt agagaaatga 1020
94 ctttagtggt attagatgtt gtggcgctat ttccatatta tgatgtacga ctttatccaa 1080
96 cgggatcaaa cccacagctt acacgtgagg tatatacaga tccgattgta tttaatccac 1140
98 cagctaattg tggactttgc cgacgttggg gtactaatcc ctataatact ttttctgagc 1200
100 tcgaaaatgc cttcattcgc ccaccacatc tttttgatag gctgaatagc ttaacaatca 1260
102 gcagtaatcg atttccagtt tcatctaatt ttatggatta ttggtcagga catacgttac 1320
104 gccgtagtta tctgaacgat tcagcagtag aagaagatag ttatggccta attacaacca 1380
106 caagagcaac aattaatccc ggagttgatg gaacaaaccg catagagtca acggcagtag 1440
108 attttcgttc tgcattgata ggtatatatg gcgtgaatag agcttctttt gtcccaggag 1500
110 gcttggttaa tggtagcact tctcctgcta atggaggatg tagagatctc tatgatacaa 1560
112 a 1561
115 <210> SEQ ID NO: 3
116 <211> LENGTH: 1554
117 <212> TYPE: DNA
118 <213> ORGANISM: Bacillus thuringiensis
121 <220> FEATURE:
122 <221> NAME/KEY: misc_feature
123 <222> LOCATION: (1146)..(1148)
124 <223> OTHER INFORMATION: Presumed translational stop codon of bTS02618A gene.
126 <400> SEQUENCE: 3
127 aaaattatcc aacatacatt tatcaaaaaag tagatgcatc ggtgttaaag ccttatacac 60
129 gctatagact agatggattt gtgaagagta gtcaagattt agaaaattgat ctcatccacc 120
131 atcataaagt ccatcttgta aaaaatgtac cagataattt agtatctgat acttactcag 180
133 atggttcttg cagcggaaatc aaccgttgtg atgaacagca tcaggtagat atgcagctag 240
135 atgcggagca tcatccaatg gattgctgtg aagcggctca aacacatgag ttttcttcct 300
137 atattaatac aggggatcta aatgcaagtg tagatcaggg catttggggtt gtattaaaag 360
139 ttcgaacaac agatgggtat gcgacgttag gaaatcttga attggtagag gttgggccat 420
141 tatcgggtga atctctagaa cggaacaaa gagataatgc gaaatggaat gcagagctag 480
143 gaagaaaacy tgcagaaata gatcgtgtgt atttagctgc gaaacaagca attaatcatc 540
145 tgttttaga ctatcaagat caacaattaa atccagaaat tgggctagca gaaattaatg 600
147 aagcttcaaa tctttagag tcaatttcgg gtgtatatag tgatacacta ttacagattc 660
149 ctgggattaa ctacgaaatt tacacagagt tatccgatcg cttacaacaa gcatcgatc 720
151 tgtatacgtc tagaaatgcg gtgcaaaatg gagactttta cagtggctta gatagttgga 780
153 atacaactat ggatgcatcg gttcagcaag atggcaatat gcatttctta gttctttcgc 840
155 attgggatgc acaagtttcc caacaattga gagtaaattc gaattgtaag tatgtcttac 900
157 gtgtgacagc aagaaaagta ggaggcggag atggatacgt cacaatccga gatggcgctc 960

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```

159 atcaccaaga aactcttaca tttaatgcat gtgactacga tgtaaatggt acgtatgtca 1020
161 atgacaattc gtatataaca gaagaagtgg tattctaccc agagacaaaa catatgtggg 1080
163 tagagggtgag tgaatccgaa ggttcattct atatagacag tattgagttt attgaaacac 1140
165 aagagtagaa gaggggggac ctaacgtata gcaactatga gaggatactc cgtacaaaca 1200
167 aagattaaaa aaaggtaaaa tgaatagaac cccctactgg tagaaggacc gatagggggg 1260
169 tcttacatga aaaaatgtag ctgtttacta aggtgtataa aaaacagcat atctgataga 1320
171 aaaaagttag taccttataa agaaagaatt ccattcacag ttctcggtatc atataaataa 1380
173 tgataggggt atccttctta ttacattat ttttcgcaat tatctcgacg ttcttctttc 1440
175 cgctcacaat gatgatgatc atgacaacaa tcgctccat agcgaactct ttcgatatta 1500
177 ataatatcta aactcgtgta gcagtcattt ccattttttt tgatccagta aata 1554
180 <210> SEQ ID NO: 4
181 <211> LENGTH: 4344
182 <212> TYPE: DNA
183 <213> ORGANISM: Bacillus thuringiensis
186 <220> FEATURE:
187 <221> NAME/KEY: CDS
188 <222> LOCATION: (668)..(4141)
189 <223> OTHER INFORMATION: Encompasses the entire sequence of SEQ ID NO:2: from
nucleotide
190 position 474 to 2034 in SEQ ID NO:4; also encompasses part of the
191 sequence of SEQ ID NO:3: from nucleotide position 2994 to
192 nucleotide position 4344 in SEQ ID NO:4; SEQ ID NO:3 shows additional
194 <220> FEATURE:
195 <223> OTHER INFORMATION: nucleotides, located downstream (3') from the sequence shown
in
196 SEQ ID NO:4 (nucleotide position 1352 to nucleotide position 1554 in
197 SEQ ID NO:3)
199 <400> SEQUENCE: 4
200 gaattcgagc tcggtacctt ttcagtgtat cgtttccctt ccatcagggt ttcaaattga 60
202 aaagccgaat gatttgaaac ttgtttacga tgtaagtcat ttgtctatga cgaaagatac 120
204 gtgtaaaaaa cgtattgaga ttgatgaatg tggacaagta gaaattgact tacaagtatt 180
206 aaagattaag ggtgtccttt cttttatcgg aaatttctct attgaacctt ttctgtgtga 240
208 aaacatgtat acaacggttg atagagatcg gtctatttcc ttaagtttcc aagatacggg 300
210 atatgtggac catattttta aatatagcgt ccaacaacta ccatattatg taattgatgg 360
212 tgatcatatt caagtacgtg atttacaat caaactgatg aaagagaatc cgcaatctgc 420
214 tcaagtatca ggtttgtttt gttttgtata tgagtaagaa ccgaagggtt gtaaaaaaga 480
216 aataggaata aatactatcc attttttcaa gaaatatttt ttattagaa aggaatcttt 540
218 cttacacggg aaaatcctaa gattgagagt aaagatatat atatataaat acaataaaga 600
220 gtttgtcagg atttttgaaa gatatgatat gaacatgcac tagatttata gtataggagg 660
222 aaaaagt atg aat cga aat aat caa aat gaa tat gaa att att gat gcc 709
223 Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala
224 1 5 10
226 ccc cat tgt ggg tgt cca tca gat gac gat gtg agg tat cct ttg gca 757
227 Pro His Cys Gly Cys Pro Ser Asp Asp Asp Val Arg Tyr Pro Leu Ala
228 15 20 25 30
230 agt gac cca aat gca gcg tta caa aat atg aac tat aaa gat tac tta 805
231 Ser Asp Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu
232 35 40 45
234 caa atg aca gat gag gac tac act gat tct tat ata aat cct agt tta 853
235 Gln Met Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu
236 50 55 60

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238	tct att agt ggt aga gat gca gtt cag act gcg ctt act gtt gtt ggg	901
239	Ser Ile Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly	
240	65 70 75	
242	aga ata ctc ggg gct tta ggt gtt ccg ttt tct gga caa ata gtg agt	949
243	Arg Ile Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser	
244	80 85 90	
246	ttt tat caa ttc ctt tta aat aca ctg tgg cca gtt aat gat aca gct	997
247	Phe Tyr Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala	
248	95 100 105 110	
250	ata tgg gaa gct ttc atg cga cag gtg gag gaa ctt gtc aat caa caa	1045
251	Ile Trp Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln	
252	115 120 125	
254	ata aca gaa ttt gca aga aat cag gca ctt gca aga ttg caa gga tta	1093
255	Ile Thr Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu	
256	130 135 140	
258	gga gac tct ttt aat gta tat caa cgt tcc ctt caa aat tgg ttg gct	1141
259	Gly Asp Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala	
260	145 150 155	
262	gat cga aat gat aca cga aat tta agt gtt gtt cgt gct caa ttt ata	1189
263	Asp Arg Asn Asp Thr Arg Asn Leu Ser Val Val Arg Ala Gln Phe Ile	
264	160 165 170	
266	gct tta gac ctt gat ttt gtt aat gct att cca ttg ttt gca gta aat	1237
267	Ala Leu Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn	
268	175 180 185 190	
270	gga cag cag gtt cca tta ctg tca gta tat gca caa gct gtg aat tta	1285
271	Gly Gln Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Val Asn Leu	
272	195 200 205	
274	cat ttg tta tta tta aaa gat gca tct ctt ttt gga gaa gga tgg gga	1333
275	His Leu Leu Leu Leu Lys Asp Ala Ser Leu Phe Gly Glu Gly Trp Gly	
276	210 215 220	
278	ttc aca cag ggg gaa att tcc aca tat tat gac cgt caa ttg gaa cta	1381
279	Phe Thr Gln Gly Glu Ile Ser Thr Tyr Tyr Asp Arg Gln Leu Glu Leu	
280	225 230 235	
282	acc gct aag tac act aat tac tgt gaa act tgg tat aat aca ggt tta	1429
283	Thr Ala Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu	
284	240 245 250	
286	gat cgt tta aga gga aca aat act gaa agt tgg tta aga tat cat caa	1477
287	Asp Arg Leu Arg Gly Thr Asn Thr Glu Ser Trp Leu Arg Tyr His Gln	
288	255 260 265 270	
290	ttc cgt aga gaa atg act tta gtg gta tta gat gtt gtg gcg cta ttt	1525
291	Phe Arg Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe	
292	275 280 285	
294	cca tat tat gat gta cga ctt tat cca acg gga tca aac cca cag ctt	1573
295	Pro Tyr Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu	
296	290 295 300	
298	aca cgt gag gta tat aca gat ccg att gta ttt aat cca cca gct aat	1621
299	Thr Arg Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn	
300	305 310 315	
302	gtt gga ctt tgc cga cgt tgg ggt act aat ccc tat aat act ttt tct	1669

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303	Val	Gly	Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	
304		320					325					330					
306	gag	ctc	gaa	aat	gcc	ttc	att	cgc	cca	cca	cat	ctt	ttt	gat	agg	ctg	1717
307	Glu	Leu	Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Asp	Arg	Leu	
308	335					340				345					350		
310	aat	agc	tta	aca	atc	agc	agt	aat	cga	ttt	cca	gtt	tca	tct	aat	ttt	1765
311	Asn	Ser	Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	
312					355				360						365		
314	atg	gat	tat	tgg	tca	gga	cat	acg	tta	cgc	cgt	agt	tat	ctg	aac	gat	1813
315	Met	Asp	Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	
316				370					375					380			
318	tca	gca	gta	caa	gaa	gat	agt	tat	ggc	cta	att	aca	acc	aca	aga	gca	1861
319	Ser	Ala	Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	
320			385						390					395			
322	aca	att	aat	ccc	gga	gtt	gat	gga	aca	aac	cgc	ata	gag	tca	acg	gca	1909
323	Thr	Ile	Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	
324		400					405					410					
326	gta	gat	ttt	cgt	tct	gca	ttg	ata	ggg	ata	tat	ggc	gtg	aat	aga	gct	1957
327	Val	Asp	Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	
328	415				420				425						430		
330	tct	ttt	gtc	cca	gga	ggc	ttg	ttt	aat	ggg	acg	act	tct	cct	gct	aat	2005
331	Ser	Phe	Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	
332					435				440					445			
334	gga	gga	tgt	aga	gat	ctc	tat	gat	aca	aat	gat	gaa	tta	cca	cca	gat	2053
335	Gly	Gly	Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	
336				450					455					460			
338	gaa	agt	acc	gga	agt	tca	acc	cat	aga	cta	tct	cat	gtt	acc	ttt	ttt	2101
339	Glu	Ser	Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	
340			465					470					475				
342	agc	ttt	caa	act	aat	cag	gct	gga	tct	ata	gct	aat	gca	gga	agt	gta	2149
343	Ser	Phe	Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	
344		480					485					490					
346	cct	act	tat	gtt	tgg	acc	cgt	cgt	gat	gtg	gac	ctt	aat	aat	acg	att	2197
347	Pro	Thr	Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	
348	495				500				505						510		
350	acc	cca	aat	aga	att	aca	caa	tta	cca	ttg	gta	aag	gca	tct	gca	cct	2245
351	Thr	Pro	Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro	
352					515				520					525			
354	gtt	tcg	ggg	act	acg	gtc	tta	aaa	ggg	cca	gga	ttt	aca	gga	ggg	ggg	2293
355	Val	Ser	Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	
356				530					535					540			
358	ata	ctc	cga	aga	aca	act	aat	ggc	aca	ttt	gga	acg	tta	aga	gta	acg	2341
359	Ile	Leu	Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr	
360			545					550					555				
362	gtt	aat	tca	cca	tta	aca	caa	caa	tat	cgc	cta	aga	gtt	cgt	ttt	gcc	2389
363	Val	Asn	Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Val	Arg	Phe	Ala	
364		560					565						570				
366	tca	aca	gga	aat	ttc	agt	ata	agg	gta	ctc	cgt	gga	ggg	gtt	tct	atc	2437
367	Ser	Thr	Gly	Asn	Phe	Ser	Ile	Arg	Val	Leu	Arg	Gly	Gly	Val	Ser	Ile	

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 12/29/2004
PATENT APPLICATION: US/10/687,879A TIME: 15:28:26

Input Set : A:\2004-12-07 2428-0125P.ST25.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; N Pos. 708

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number

L:82 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:660